

Application No 08/881589  
NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE-SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.321 - 1.325 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.321-1.325. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.321(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.321(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.322 and/or 1.323, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.325(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.321(e).
- ☐ 7. Other: \_\_\_\_\_

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.321(a) or 1.321(f) or 1.321(g) or 1.325(b) or 1.325(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216  
For CRF Submission Help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

A. Decoux

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5-9-00  
A.6

1644

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/08/881,509C  
DATE: 05/09/2000  
TIME: 15:48:42

Input Set : A:\5647015.app  
Output Set: N:\CRF3\05092000\H881509C.raw

ENTERED

5 (1) GENERAL INFORMATION:  
C--> 7 (i) APPLICANT: SCHENDEL, Dolores J.  
C--> 9 (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA  
C--> 11 (iii) NUMBER OF SEQUENCES: 45  
C--> 13 (iv) CORRESPONDENCE ADDRESS:  
C--> 14 (A) ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP  
C--> 15 (B) STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby  
C--> 16 (C) CITY: Washington  
C--> 17 (D) STATE: DC  
C--> 18 (E) COUNTRY: USA  
C--> 19 (F) ZIP: 20005-5701  
C--> 21 (v) COMPUTER READABLE FORM:  
C--> 22 (A) MEDIUM TYPE: Floppy disk  
C--> 23 (B) COMPUTER: IBM PC compatible  
C--> 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
C--> 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
C--> 27 (vi) CURRENT APPLICATION DATA:  
C--> 28 (A) APPLICATION NUMBER: US/08/881,509C  
C--> 29 (B) FILING DATE: 24-Jun-1997  
C--> 30 (C) CLASSIFICATION:  
C--> 32 (viii) ATTORNEY/AGENT INFORMATION:  
C--> 33 (A) NAME: Kitts, Monica Chin  
C--> 34 (B) REGISTRATION NUMBER: 36,105  
C--> 35 (C) REFERENCE/DOCKET NUMBER: 564-7015  
C--> 37 (ix) TELECOMMUNICATION INFORMATION:  
C--> 38 (A) TELEPHONE: (202) 638-5000  
C--> 39 (B) TELEFAX: (202) 638-4810  
42 (2) INFORMATION FOR SEQ ID NO: 1:  
C--> 44 (i) SEQUENCE CHARACTERISTICS:  
C--> 45 (A) LENGTH: 1341 base pairs  
C--> 46 (B) TYPE: nucleic acid  
C--> 47 (C) STRANDEDNESS: both  
C--> 48 (D) TOPOLOGY: linear  
C--> 50 (ix) FEATURE:  
C--> 51 (A) NAME/KEY: CDS  
C--> 52 (B) LOCATION:1..801  
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C--> 56 (B) LOCATION:1..54  
C--> 58 (ix) FEATURE:  
C--> 59 (A) NAME/KEY: mat\_peptide  
C--> 60 (B) LOCATION:55..801  
C--> 62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
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65 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu  
66 -18 -15 -10 -5  
68 AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA 96

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509C

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70				1			5					10					
72	CAA	GAA	GTG	AAC	ATA	ACC	TGT	AGC	CAC	AAC	AAC	ATT	GCT	ACA	AAT	GAT	144
73	Gln	Glu	Val	Asn	Ile	Thr	Cys	Ser	His	Asn	Asn	Ile	Ala	Thr	Asn	Asp	
74	15				20					25						30	
76	TAT	ATC	ACG	TGG	TAC	CAA	CAG	TTT	CCC	AGC	CAA	GGA	CCA	CGA	TTT	ATT	192
77	Tyr	Ile	Thr	Trp	Tyr	Gln	Gln	Phe	Pro	Ser	Gln	Gly	Pro	Arg	Phe	Ile	
78				35						40					45		
80	ATT	CAA	GGA	TAC	AAG	ACA	AAA	GTT	ACA	AAC	GAA	GTG	GCC	TCC	CTG	TTT	240
81	Ile	Gln	Gly	Tyr	Lys	Thr	Lys	Val	Thr	Asn	Glu	Val	Ala	Ser	Leu	Phe	
82				50					55					60			
84	ATC	CCT	GCC	GAC	AGA	AAG	TCC	AGC	ACT	CTG	AGC	CTG	CCC	CGG	GTT	TCC	288
85	Ile	Pro	Ala	Asp	Arg	Lys	Ser	Ser	Thr	Leu	Ser	Leu	Pro	Arg	Val	Ser	
86			65				70					75					
88	CTG	AGC	GAC	ACT	GCT	GTG	TAC	TAC	TGC	CTC	GTG	GGT	GGT	TCT	GCA	AGG	336
89	Leu	Ser	Asp	Thr	Ala	Val	Tyr	Cys	Leu	Val	Gly	Gly	Ser	Ala	Arg		
90	80				85				90								
92	CAA	CTG	ACC	TTT	GGA	TCT	GGG	ACA	CAA	TTG	ACT	GTT	TTA	CCT	GAT	ATC	384
93	Gln	Leu	Thr	Phe	Gly	Ser	Gly	Thr	Gln	Leu	Thr	Val	Leu	Pro	Asp	Ile	
94	95				100					105					110		
96	CAG	AAC	CCT	GAC	CCT	GCC	GTG	TAC	CAG	CTG	AGA	GAC	TCT	AAA	TCC	AGT	432
97	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	
98				115					120					125			
100	GAC	AAG	TCT	GTC	TGC	CTA	TTC	ACC	GAT	TTT	GAT	TCT	CAA	ACA	AAT	GTG	480
101	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	
102				130					135					140			
104	TCA	CAA	AGT	AAG	GAT	TCT	GAT	GTG	TAT	ATC	ACA	GAC	AAA	ACT	GTG	CTA	528
105	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr	Val	Leu	
106			145				150					155					
108	GAC	ATG	AGG	TCT	ATG	GAC	TTC	AAG	AGC	AAC	AGT	GCT	GTG	GCC	TGG	AGC	576
109	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	
110	160					165					170						
112	AAC	AAA	TCT	GAC	TTT	GCA	TGT	GCA	AAC	GCC	TTC	AAC	AAC	AGC	ATT	ATT	624
113	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	
114	175				180					185					190		
116	CCA	GAA	GAC	ACC	TTC	TTC	CCC	AGC	CCA	GAA	AGT	TCC	TGT	GAT	GTC	AAG	672
117	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	
118				195					200					205			
120	CTG	GTC	GAG	AAA	AGC	TTT	GAA	ACA	GAT	ACG	AAC	CTA	AAC	TTT	CAA	AAC	720
121	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	
122			210						215					220			
124	CTG	TCA	GTG	ATT	GGG	TTC	CGA	ATC	CTC	CTC	CTG	AAA	GTG	GCC	GGG	TTT	768
125	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	
126			225				230					235					
128	AAT	CTG	CTC	ATG	ACG	CTG	CGG	CTG	TGG	TCC	AGC	TGAGATCTGC	AAGATTGTAA				821
129	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser						
130	240					245											
132	GACAGCCTGT	GCTCCCTCGC	TCCTTCCTCT	GCATTGCCCC	TCTTCTCCCT	CTCCAAACAG											881
134	AGGGAACCTCT	CCTACCCCA	AGGAGGTGAA	AGCTGTACC	ACCTCTGTGC	CCCCCGGCA											941

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136 ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA 1001
138 CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA 1061
140 GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCTC TCCTGCTCCC CAGAGACTGC 1121
142 CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCTGGAG 1181
144 AATGTGTGTA GGGGTTTATT TTTTTTAAT AGTGTTTATA AAGAAATACA TAGTATCTTT 1241
146 CTTCTCAAGA CGTGGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG 1301
148 GCGGTGTGTG ATGTCCTGCT GCCGATGCCT TCATTTAAAT 1341
151 (2) INFORMATION FOR SEQ ID NO: 2:
C--> 153 (i) SEQUENCE CHARACTERISTICS:
C--> 154 (A) LENGTH: 267 amino acids
C--> 155 (B) TYPE: amino acid
C--> 156 (D) TOPOLOGY: linear
C--> 158 (ii) MOLECULE TYPE: protein
C--> 160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
162 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
163 -18 -15 -10 -5
165 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
166 1 5 10
168 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
169 15 20 25 30
171 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
172 35 40 45
174 Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
175 50 55 60
177 Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
178 65 70 75
180 Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
181 80 85 90
183 Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
184 95 100 105 110
186 Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
187 115 120 125
189 Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
190 130 135 140
192 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
193 145 150 155
195 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
196 160 165 170
198 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
199 175 180 185 190
201 Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
202 195 200 205
204 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
205 210 215 220
207 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
208 225 230 235
210 Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
211 240 245
214 (2) INFORMATION FOR SEQ ID NO: 3:

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509C

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Output Set: N:\CRF3\05092000\H881509C.raw

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C--> 216      (i) SEQUENCE CHARACTERISTICS:
C--> 217          (A) LENGTH: 936 base pairs
C--> 218          (B) TYPE: nucleic acid
C--> 219          (C) STRANDEDNESS: both
C--> 220          (D) TOPOLOGY: linear
C--> 222      (ix) FEATURE:
C--> 223          (A) NAME/KEY: CDS
C--> 224          (B) LOCATION:1..933
C--> 226      (ix) FEATURE:
C--> 227          (A) NAME/KEY: sig_peptide
C--> 228          (B) LOCATION:1..63
C--> 230      (ix) FEATURE:
C--> 231          (A) NAME/KEY: mat_peptide
C--> 232          (B) LOCATION:64..933
C--> 234      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
236 ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA      48
237 Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
238 -21 -20 -15 -10
240 GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA      96
241 Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
242 -5 1 5 10
244 CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC      144
245 Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
246 15 20 25
248 TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT      192
249 Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
250 30 35 40
252 CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC      240
253 Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
254 45 50 55
256 GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG      288
257 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
258 60 65 70 75
260 AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC      336
261 Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
262 80 85 90
264 AGC AGC GAA ACT AAC TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG      384
265 Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
266 95 100 105
268 CTC ACG GTC ACA GAG GAC CTG AAA AAC GTG TTC CCA CCC GAG GTC GCT      432
269 Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
270 110 115 120
272 GTG TTT GAG CCA TCA GAA GCA GAG ATC TCC CAC ACC CAA AAG GCC ACA      480
273 Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
274 125 130 135
276 CTG GTG TGC CTG GCC ACA GGC TTC TAC CCC GAC CAC GTG GAG CTG AGC      528
277 Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
278 140 145 150 155
280 TGG TGG GTG AAT GGG AAG GAG GTG CAC AGT GGG GTC AGC ACA GAC CCG      576

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000

TIME: 15:48:42

Input Set : A:\5647015.app

Output Set: N:\CRF3\05092000\H881509C.raw

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281 Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
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284 CAG CCC CTC AAG GAG CAG CCC GCC CTC AAT GAC TCC AGA TAC TGC CTG      624
285 Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
286      175      180      185
288 AGC AGC CGC CTG AGG GTC TCG GCC ACC TTC TGG CAG AAC CCC CGC AAC      672
289 Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
290      190      195      200
292 CAC TTC CGC TGT CAA GTC CAG TTC TAC GGG CTC TCG GAG AAT GAC GAG      720
293 His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
294      205      210      215
296 TGG ACC CAG GAT AGG GCC AAA CCT GTC ACC CAG ATC GTC AGC GCC GAG      768
297 Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
298      220      225      230      235
300 GCC TGG GGT AGA GCA GAC TGT GGC TTC ACC TCC GAG TCT TAC CAG CAA      816
301 Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
302      240      245      250
304 GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC TTG CTA GGG AAG GCC      864
305 Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
306      255      260      265
308 ACC TTG TAT GCC GTG CTG GTC AGT GCC CTC GTG CTG ATG GCC ATG GTC      912
309 Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
310      270      275      280
312 AAG AGA AAG GAT TCC AGA GGC TAG      936
313 Lys Arg Lys Asp Ser Arg Gly
314      285      290
317 (2) INFORMATION FOR SEQ ID NO: 4:
C--> 319      (i) SEQUENCE CHARACTERISTICS:
C--> 320          (A) LENGTH: 311 amino acids
C--> 321          (B) TYPE: amino acid
C--> 322          (D) TOPOLOGY: linear
C--> 324      (ii) MOLECULE TYPE: protein
C--> 326      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
328 Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
329 -21 -20      -15      -10
331 Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
332 -5      1      5      10
334 Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
335      15      20      25
337 Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
338      30      35      40
340 Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
341      45      50      55
343 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
344      60      65      70      75
346 Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
347      80      85      90
349 Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
350      95      100      105

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000

TIME: 15:48:43

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Output Set: N:\CRF3\05092000\H881509C.raw

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L:11 M:220 C: Keyword misspelled, [(iii) NUMBER OF SEQUENCES:]  
L:13 M:220 C: Keyword misspelled, [(iv) CORRESPONDENCE ADDRESS:]  
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L:15 M:220 C: Keyword misspelled, [(B) STREET:]  
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L:23 M:220 C: Keyword misspelled, [(B) COMPUTER:]  
L:24 M:220 C: Keyword misspelled, [(C) OPERATING SYSTEM:]  
L:25 M:220 C: Keyword misspelled, [(D) SOFTWARE:]  
L:27 M:220 C: Keyword misspelled, [(vi) CURRENT APPLICATION DATA:]  
L:28 M:220 C: Keyword misspelled, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled, [(B) FILING DATE:]  
L:30 M:220 C: Keyword misspelled, [(C) CLASSIFICATION:]  
L:32 M:220 C: Keyword misspelled, [(vii) ATTORNEY/AGENT INFORMATION:]  
L:33 M:220 C: Keyword misspelled, [(A) NAME:]  
L:34 M:220 C: Keyword misspelled, [(B) REGISTRATION NUMBER:]  
L:35 M:220 C: Keyword misspelled, [(C) REFERENCE/DOCKET NUMBER:]  
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L:39 M:220 C: Keyword misspelled, [(B) TELEFAX:]  
L:44 M:220 C: Keyword misspelled, [(i) SEQUENCE CHARACTERISTICS:]  
L:45 M:220 C: Keyword misspelled, [(A) LENGTH:]  
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L:48 M:220 C: Keyword misspelled, [(D) TOPOLOGY:]  
L:50 M:220 C: Keyword misspelled, [(ix) FEATURE:]  
L:51 M:220 C: Keyword misspelled, [(A) NAME/KEY:]  
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L:54 M:220 C: Keyword misspelled, [(ix) FEATURE:]  
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L:59 M:220 C: Keyword misspelled, [(A) NAME/KEY:]  
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L:62 M:220 C: Keyword misspelled, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
L:153 M:220 C: Keyword misspelled, [(i) SEQUENCE CHARACTERISTICS:]  
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L:155 M:220 C: Keyword misspelled, [(B) TYPE:]  
L:156 M:220 C: Keyword misspelled, [(D) TOPOLOGY:]  
L:158 M:220 C: Keyword misspelled, [(ii) MOLECULE TYPE:]  
L:160 M:220 C: Keyword misspelled, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
L:216 M:220 C: Keyword misspelled, [(i) SEQUENCE CHARACTERISTICS:]

## VERIFICATION SUMMARY

PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000

TIME: 15:48:43

Input Set : A:\5647015.app

Output Set: N:\CRF3\05092000\H881509C.raw

L:217 M:220 C: Keyword misspelled, [(A) LENGTH:]  
L:218 M:220 C: Keyword misspelled, [(B) TYPE:]  
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:507 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
L:609 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:643 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23, Value=[not relevant]  
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:715 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24, Value=[not relevant]  
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:737 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25, Value=[not relevant]  
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:759 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26, Value=[not relevant]  
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:781 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27, Value=[not relevant]  
L:797 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28, Value=[not relevant]  
L:813 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29, Value=[not relevant]  
L:829 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30, Value=[not relevant]  
L:845 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=31, Value=[not relevant]  
L:861 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32, Value=[not relevant]  
L:877 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=33, Value=[not relevant]  
L:893 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=34, Value=[not relevant]  
L:909 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=35, Value=[not relevant]  
L:925 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=36, Value=[not relevant]  
L:941 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=37, Value=[not relevant]  
L:957 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=38, Value=[not relevant]  
L:973 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=39, Value=[not relevant]  
L:989 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=40, Value=[not relevant]  
L:1005 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=41, Value=[not relevant]  
L:1021 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=42, Value=[not relevant]  
L:1037 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=43, Value=[not relevant]  
L:1053 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=44, Value=[not relevant]  
L:1068 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=45, Value=[not relevant]  
L:1080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45